

1647 #11

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FEB 08 2001

TECH CENTER 1600/2900

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/510,332 DATE: 01/31/2001  
 TIME: 13:36:28

Input Set : A:\Uc-980-1.TXT  
 Output Set: N:\CRF3\01312001\I510332.raw

3 <110> APPLICANT: Zuker, Charles S.  
 4 Adler, Jon Elliot  
 5 Ryba, Nick  
 6 Mueller, Ken  
 7 Hoon, Mark  
 8 The Regents of the University of California  
 10 <120> TITLE OF INVENTION: T2R, a Novel Family of Taste Receptors  
 12 <130> FILE REFERENCE: 02307E-098010US  
 14 <140> CURRENT APPLICATION NUMBER: US 09/510,332  
 15 <141> CURRENT FILING DATE: 2000-02-22  
 17 <150> PRIOR APPLICATION NUMBER: US 09/393,634  
 18 <151> PRIOR FILING DATE: 1999-09-10  
 20 <160> NUMBER OF SEQ ID NOS: 172  
 22 <170> SOFTWARE: PatentIn Ver. 2.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 299  
 26 <212> TYPE: PRT  
 27 <213> ORGANISM: Homo sapiens  
 29 <220> FEATURE:  
 30 <223> OTHER INFORMATION: human T2R01 (hGR01)  
 32 <400> SEQUENCE: 1  
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 36 Phe Leu Leu Gly Ile Phe Thr Asn Gly Ile Ile Val Val Val Asn Gly  
 37 20 25 30  
 39 Ile Asp Leu Ile Lys His Arg Lys Met Ala Pro Leu Asp Leu Leu Leu  
 40 35 40 45  
 42 Ser Cys Leu Ala Val Ser Arg Ile Phe Leu Gln Leu Phe Ile Phe Tyr  
 43 50 55 60  
 45 Val Asn Val Ile Val Ile Phe Phe Ile Glu Phe Ile Met Cys Ser Ala  
 46 65 70 75 80  
 48 Asn Cys Ala Ile Leu Leu Phe Ile Asn Glu Leu Glu Leu Trp Leu Ala  
 49 85 90 95  
 51 Thr Trp Leu Gly Val Phe Tyr Cys Ala Lys Val Ala Ser Val Arg His  
 52 100 105 110  
 54 Pro Leu Phe Ile Trp Leu Lys Met Arg Ile Ser Lys Leu Val Pro Trp  
 55 115 120 125  
 57 Met Ile Leu Gly Ser Leu Leu Tyr Val Ser Met Ile Cys Val Phe His  
 58 130 135 140  
 60 Ser Lys Tyr Ala Gly Phe Met Val Pro Tyr Phe Leu Arg Lys Phe Phe  
 61 145 150 155 160  
 63 Ser Gln Asn Ala Thr Ile Gln Lys Glu Asp Thr Leu Ala Ile Gln Ile  
 64 165 170 175  
 66 Phe Ser Phe Val Ala Glu Phe Ser Val Pro Leu Leu Ile Phe Leu Phe  
 67 180 185 190  
 69 Ala Val Leu Leu Leu Ile Phe Ser Leu Gly Arg His Thr Arg Gln Met  
 70 195 200 205

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72 Arg Asn Thr Val Ala Gly Ser Arg Val Pro Gly Arg Gly Ala Pro Ile
73      210      215      220
75 Ser Ala Leu Leu Ser Ile Leu Ser Phe Leu Ile Leu Tyr Phe Ser His
76 225      230      235      240
78 Cys Met Ile Lys Val Phe Leu Ser Ser Leu Lys Phe His Ile Arg Arg
79      245      250      255
81 Phe Ile Phe Leu Phe Phe Ile Leu Val Ile Gly Ile Tyr Pro Ser Gly
82      260      265      270
84 His Ser Leu Ile Leu Ile Leu Gly Asn Pro Lys Leu Lys Gln Asn Ala
85      275      280      285
87 Lys Lys Phe Leu Leu His Ser Lys Cys Cys Gln
88      290      295
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92 <211> LENGTH: 900
93 <212> TYPE: DNA
94 <213> ORGANISM: Homo sapiens
96 <220> FEATURE:
97 <223> OTHER INFORMATION: human T2R01 (hGR01)
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101 attttcacaa atggcatcat tgtggtggtg aatggcattg acttgatcaa gcacagaaaa 120
102 atggctccgc tggatctcct tcttcttctt ctggcagttt ctagaatttt tctgcagttg 180
103 ttcattctct acgttaagt gattgttata ttcttcatag aattcatcat gtgttctgcg 240
104 aattgtgcaa ttctcttatt tataaatgaa ttggaacttt ggcttgccac atggctcggc 300
105 gttttctatt gtgccaaagt tggcagcgtc cgtcaccac tcttcatctg gttgaagatg 360
106 aggatatcca agctggctcc atggatgata ctgggggtct tgctatatgt atctatgatt 420
107 tgtgttttcc atagcaata tgcagggttt atgggtccat acttcctaag gaaatttttc 480
108 tccccaaatg ccacaattca aaaagaagat acactggcta tacagatttt ctcttttgtt 540
109 gctgagttct cagtgccatt gcttatcttc ctttttgcgt ttttgctctt gattttctct 600
110 ctggggaggg acaccgggca aatgagaaac acagtggccg gcagcagggg tccctggcagg 660
111 ggtgcaccca tcagcgcgtt gctgtctata ctgtccttcc tgatctctta cttctccac 720
112 tgcattgata aagtttttct ctcttctcta aagtttcaca tcagaagggt catctttctg 780
113 ttcttcatcc ttgtgattg tatataacct tctggacact ctctcatctt aatttttaga 840
114 aatcctaaat tgaaacaaaa tgcaaaaaag ttctctctcc acagtaagtg ctgtcagtg 900
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125 <220> FEATURE:
126 <221> NAME/KEY: MOD_RES
127 <222> LOCATION: (143)
128 <223> OTHER INFORMATION: Xaa = any amino acid
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134 Glu Phe Phe Thr Gly Ile Thr Val Asn Gly Phe Leu Ile Ile Val Asn
135      20      25      30

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137 Cys Asn Glu Leu Ile Lys His Arg Lys Leu Met Pro Ile Gln Ile Leu  
 138 35 40 45  
 140 Leu Met Cys Ile Gly Met Ser Arg Phe Gly Leu Gln Met Val Leu Met  
 141 50 55 60  
 143 Val Gln Ser Phe Phe Ser Val Phe Phe Pro Leu Leu Tyr Val Lys Ile  
 144 65 70 75 80  
 146 Ile Tyr Gly Ala Ala Met Met Phe Leu Trp Met Phe Phe Ser Ser Ile  
 147 85 90 95  
 149 Ser Leu Trp Phe Ala Thr Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile  
 150 100 105 110  
 152 Ser Gly Phe Thr Gln Ser Cys Phe Leu Trp Leu Lys Phe Arg Ile Pro  
 153 115 120 125 /  
 W-155 Lys Leu Ile Pro Trp Leu Phe Trp Glu Ala Phe Trp Pro Leu Xaa Ala  
 156 130 135 140  
 158 Leu His Leu Cys Val Glu Val Asp Tyr Ala Lys Asn Val Glu Glu Asp  
 159 145 150 155 160  
 161 Ala Leu Arg Asn Thr Leu Lys Lys Ser Lys Thr Lys Ile Lys Lys  
 162 165 170 175  
 164 Ile Ser Glu Val Leu Leu Val Asn Leu Ala Leu Ile Phe Pro Leu Ala  
 165 180 185 190  
 167 Ile Phe Val Met Cys Thr Ser Met Leu Leu Ile Ser Leu Tyr Lys His  
 168 195 200 205  
 170 Thr His Arg Met Gln His Gly Ser His Gly Phe Arg Asn Ala Asn Thr  
 171 210 215 220  
 173 Glu Ala His Ile Asn Ala Leu Lys Thr Val Ile Thr Phe Phe Cys Phe  
 174 225 230 235 240  
 176 Phe Ile Ser Tyr Phe Ala Ala Phe Met Thr Asn Met Thr Phe Ser Leu  
 177 245 250 255  
 179 Pro Tyr Arg Ser His Gln Phe Phe Met Leu Lys Asp Ile Met Ala Ala  
 180 260 265 270  
 182 Tyr Pro Ser Gly His Ser Val Ile Ile Leu Ser Asn Ser Lys Phe  
 183 275 280 285  
 185 Gln Gln Ser Phe Arg Arg Ile Leu Cys Leu Lys Lys Lys Leu  
 186 290 295 300  
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 192 <213> ORGANISM: Homo sapiens  
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 195 <223> OTHER INFORMATION: human T2R02 (hGR02)  
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 198 <223> OTHER INFORMATION: human T2R02 (hGR02)  
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 202 gggatcacag taaatggatt tcttatcatt gttactgta atgaattgat caaacataga 120  
 203 aagctaattgc caattcaaatt cctcttaattg tgcataggga tgtctagatt tggctctgag 180  
 204 atggtgttaa tgggtacaaag ttttttctct gtgttcttct cactccttta cgtcaaaaata 240  
 205 atttatgggtg cagcaatgat gttcctttgg atgtttttta gctctatcag cctatgggttt 300  
 206 gccacttgcc tttctgtatt ttactgcctc aagatttcag gcttccactca gtcctgtttt 360

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207 ctttggttga aattcaggat cccaaagtta ataccttggc tgcttctggg aagcgttctg 420
208 gcctctgtga gcattgcac tggtgtgcga ggtagattac gctaaaaatg tggagagga 480
209 tgccctcaga aacaccacac taaaaaagag taaaacaaag ataaagaaaa ttagtgaggt 540
210 gcttctgtgc aacttggcat taatatttcc tctagccata tttgtgatgt gcacttctat 600
211 gttactcacc tctctttaca agcacactca tgggatgcaa catggatctc atggctttag 660
212 aaatgccaac acagaagccc atataaatgc attaaaaaca gtgataacat tcttttgctt 720
213 ctttatttct tattttgctg ctttcacgac aaatatgaca tttagtttac cttacagaag 780
214 tcaccagttc tttatgctga aggacataat ggcagcatat cctctggcc actcggttat 840
215 aataatcttg agtaattcta agttccaaca atcatttaga agaattctct gcctcaaaaa 900
216 gaaactatga                                     910
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220 <211> LENGTH: 316
221 <212> TYPE: PRP
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224 <220> FEATURE:
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232   20              25              30
234 Ser Ser Trp Phe Lys Thr Lys Arg Met Ser Leu Ser Asp Phe Ile Ile
235   35              40              45
237 Thr Thr Leu Ala Leu Leu Arg Ile Ile Leu Leu Cys Ile Ile Leu Thr
238   50              55              60
240 Asp Ser Phe Leu Ile Glu Phe Ser Pro Asn Thr His Asp Ser Gly Ile
241   65              70              75              80
243 Ile Met Gln Ile Ile Asp Val Ser Trp Thr Phe Thr Asn His Leu Ser
244   85              90              95
246 Ile Trp Leu Ala Thr Cys Leu Gly Val Leu Tyr Cys Leu Lys Ile Ala
247  100             105             110
249 Ser Phe Ser His Pro Thr Phe Leu Trp Leu Lys Trp Arg Val Ser Arg
250  115             120             125
252 Val Met Val Trp Met Leu Leu Gly Ala Leu Leu Leu Ser Cys Gly Ser
253  130             135             140
255 Thr Ala Ser Leu Ile Asn Glu Phe Lys Leu Tyr Ser Val Phe Arg Gly
256 145             150             155             160
258 Ile Glu Ala Thr Arg Asn Val Thr Glu His Phe Arg Lys Lys Arg Ser
259 165             170             175
261 Glu Tyr Tyr Leu Ile His Val Leu Gly Thr Leu Trp Tyr Leu Pro Pro
262 180             185             190
264 Leu Ile Val Ser Leu Ala Ser Tyr Ser Leu Leu Ile Phe Ser Leu Gly
265 195             200             205
267 Arg His Thr Arg Gln Met Leu Gln Asn Gly Thr Ser Ser Arg Asp Pro
268 210             215             220
270 Thr Thr Glu Ala His Lys Arg Ala Ile Arg Ile Ile Leu Ser Phe Phe
271 225             230             235             240
273 Phe Leu Phe Leu Leu Tyr Phe Leu Ala Phe Leu Ile Ala Ser Phe Gly
274 245             250             255

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276 Asn Phe Leu Pro Lys Thr Lys Met Ala Lys Met Ile Gly Glu Val Met  
 277 260 265 270  
 279 Thr Met Phe Tyr Pro Ala Gly His Ser Phe Ile Leu Ile Leu Gly Asn  
 280 275 280 285  
 282 Ser Lys Leu Lys Gln Thr Phe Val Val Met Leu Arg Cys Glu Ser Gly  
 283 290 295 300  
 285 His Leu Lys Pro Gly Ser Lys Gly Pro Ile Phe Ser  
 286 305 310 315  
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 290 <211> LENGTH: 951  
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 292 <213> ORGANISM: Homo sapiens  
 294 <220> FEATURE:  
 295 <223> OTHER INFORMATION: human T2R03 (hGR03)  
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 299 attctgggtca attgtttcat tgagtttggtc aatggtagca gctgggtcaa gaccaagaga 120  
 300 atgtctttgt ctgacttcat catcaccacc ctggcactct tgaggatcat tctgtgtgt 180  
 301 attatcttga ctgatatgtt tttaatagaa ttctctccca acacacatga ttcagggata 240  
 302 ataattgcaaa ttattgatgt ttcttggaca ttacaaaacc atctgagcat ttggcttgc 300  
 303 acctgtcttg gtgtctctta ctgctgaaa atcgccagtt tctctcacc caccattctc 360  
 304 tggctcaagt ggagagtttc taggtgatg gtatggatgc tgttgggtgc actgctctta 420  
 305 tctgttggtg gtaccgcac tctgatcaat gagtttaagc tctattctgt ctttagggga 480  
 306 attgaggcca ccaggaatgt gactgaacac tlcagaaaaga agaggagtga gtattatctg 540  
 307 atccatgttc ttgggactct gtggtacctg cctcccttaa ttgtgtccct ggcctctac 600  
 308 tcttttctca tcttctccct ggggaggcac acacggcaga tcttgcaaaa tgggacaagc 660  
 309 tccagagatc caaccactga ggcaccacaag agggccatca gaatcctct ttccttcttc 720  
 310 tttctcttct tactttactt tcttcttct ttaattgcat catttggtta ttctctacca 780  
 311 aaaaccaaga tggtctaat gattggcgaa gtaatgacaa tgttttatcc tgetggccac 840  
 312 tcatcttatt tcattctggg gaacagtaag ctgaagcaga catttgtagt gatgtcccg 900  
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 317 <211> LENGTH: 299  
 318 <212> TYPE: PRT  
 319 <213> ORGANISM: Homo sapiens  
 321 <220> FEATURE:  
 322 <223> OTHER INFORMATION: human T2R04 (hGR04)  
 324 <400> SEQUENCE: 7  
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 328 Asn Phe Val Gly Ile Ile Met Asn Leu Phe Ile Thr Val Val Asn Cys  
 329 20 25 30  
 331 Lys Thr Trp Val Lys Ser His Arg Ile Ser Ser Ser Asp Arg Ile Leu  
 332 35 40 45  
 334 Phe Ser Leu Gly Ile Thr Arg Phe Leu Met Leu Gly Leu Phe Leu Val  
 335 50 55 60  
 337 Asn Thr Ile Tyr Phe Val Ser Ser Asn Thr Glu Arg Ser Val Tyr Leu  
 338 65 70 75 80  
 340 Ser Ala Phe Phe Val Leu Cys Phe Met Phe Leu Asp Ser Ser Ser Val

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FYI:

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\Uc-980-1.TXT

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L:531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:537 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
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L:1091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
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L:1895 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39  
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L:1937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:1955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41  
L:1956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41  
L:1957 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41  
L:1958 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41  
L:1959 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41  
L:1961 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41  
L:1963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41

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L:1965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41  
L:1985 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42